

GenCore version 5.1.4\_p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 23:36:55 ; Search time 2268 seconds  
(without alignments)

12339.418 Million cell updates/sec

Title: US-09-847-081b-1

Perfect score: 1728  
Sequence: 1 agaaaccagaagaacaac.....tcatcaaacctcaagtga 1728

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_estin:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estro:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vit:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_pro:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	655.4	37.9	781	14	BQ511016
2	621.6	36.0	751	14	BQ046203
3	605.2	35.0	787	13	BM410846
4	568.4	32.9	677	12	BG351357
5	552.2	32.0	686	10	AW442101
6	551.2	31.9	785	13	BM408984

7	541.2	31.3	682	13	BM409200
8	532.8	30.8	672	10	AW442407
9	522	30.2	642	10	BE433198
10	515.8	29.8	676	10	AW222027
11	498.2	28.8	634	13	BM412533
12	487.2	28.2	598	13	BI921390
13	486.4	28.1	600	10	BE460889
14	483.4	28.0	623	10	BE432511
15	478.8	27.7	685	10	AW221932
16	473.2	27.4	582	10	AW223316
17	466.8	27.0	582	10	AW223666
18	466.4	27.0	581	10	BE432955
19	466.4	27.0	623	13	BM536249
20	461	26.7	791	10	AW223528
21	458.4	26.5	573	10	BE435308
22	458.4	26.5	605	10	BE435064
23	458.2	26.5	585	10	AW222245
24	458	26.5	1655	11	AY111032
25	457.8	26.5	585	10	BE432595
26	453.2	26.2	562	10	BE433966
27	449.4	26.0	581	10	AW222806
28	442.4	25.6	556	10	AW222152
29	439.6	25.4	542	10	BE431550
30	439	25.4	543	13	BM411875
31	437.4	25.3	634	10	AW441216
32	435	25.2	555	10	BE460463
33	434.4	25.1	566	12	BF112979
34	431.6	25.0	542	10	BE432248
35	429.2	24.8	563	10	BE461396
36	427.8	24.8	580	10	AW092690
37	427.6	24.7	563	10	BE437095
38	426.8	24.7	536	10	BE434911
39	425.4	24.6	558	10	AW222427
40	425.4	24.6	1201	11	AY108547
41	424.2	24.5	744	13	BM412719
42	423.6	24.5	551	10	BE432084
43	415.2	24.0	536	10	AW223238
44	409.2	23.7	519	10	BE433537
45	405.2	23.4	717	10	AW223529

## ALIGNMENTS

RESULT 1  
BQ511016/c  
LOCUS  
DEFINITION  
BQ511016  
BQ511016.2  
GI:21926690  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

781 bp mRNA linear EST 22-JUL-2002  
Generation of a set of potato cDNA clones for microarray  
analyses mixed potato tissues Solanum tuberosum cDNA clone STM067  
3' end, mRNA sequence.

potato.

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 781)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,

Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and

Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses

Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21369885.

Other ESTs: EST618430

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Email: potato@igrr.org

This clone is available through the Research Genetics, contact the

Research Genetics for further information 1-800-711-6195 or

cdna@resgen.com

Db 62 TCTCCCCACTAGCAAAACATGAATGAAGTTTTTGA 26

RESULT 2  
BQ046203  
LOCUS  
DEFINITION  
EST595321 P. infestans-challenged potato leaf, incompatible reaction Solanum tuberosum cDNA clone BPLI14E21 5' end, mRNA sequence.  
751 bp mRNA linear EST 29-MAR-2002  
BQ046203.1 GI:19820189  
potato.  
EST.  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Zhang,P., Hernandez,M., Tornqvist,C.-E., Wirtz,U., Loukolanov,A., Rangel,P., Haberlach,G.T., Karanycheva,S.A., Tsai,J., Chienmingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Helgeson,J. and Baker,B.  
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, incompatible interaction (2002)  
Unpublished (2002)  
Contact: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: cdna@resgen.com  
For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: T3.  
Location/Qualifiers  
1..751  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="BPLI14E21"  
/clone\_lib="P. infestans-challenged potato leaf,  
incompatible reaction"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: UC Berkeley, PGEC; sequencing: The  
Institute for Genomic Research. Whole plants were  
challenged with 450,000 sporangia/ml P. infestans isolate  
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf  
tissue was collected at 1, 2, 5, 12, and 24 hours  
post-challenge and frozen in liquid nitrogen immediately  
upon removal. Kennebec plants showed no signs of HR.  
Katahdin plants (susceptible to P. infestans US-1) were  
used as controls and showed infection. NOTE: We cannot  
exclude the possibility that this sequence is actually  
derived from Phytophthora rather than potato."  
219 a. 119 c 214 t

BASE COUNT  
ORIGIN  
Query Match 36.0%; Score 621.6; DB 14; Length 751;  
Best Local Similarity 91.8%; Pred.No.2.3e-163; Indels 3; Gaps 3;  
Matches 690; Conservative 0; Mismatches 59;

Qy 438 AATTGCTGATCCAGATATTTCATCGTTGGGTGGATCAAGAAGCTGAAAAGGGAAGCATT 497  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 AAATGCAGATTGAGATATTCGTTGTAGGAAGATCAAGAAGCTGAGATGGAAGGAGTT 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 498 CTCGTGACAGTCCAGTTTGTTGGGTAGCCCAGCTGGAGAAATGACTGTGTCATCAGAGAA 557  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 TTCTGTACAGTCCAGTTTGTTGGGTAGTCCAGCTGGAGAAATGGCTGTGTCATCAGAGAA 120  
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Qy 558 AAAAGGTATCATGTGCTATTAAAGCAGGCCAGCTTTAGTGAAGGCCAGCTGAGATCTAC 617  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 AAAGGTGTATGAGTGGTATTGTAAGCAGGCCAGCTTTAGTGAAGGCCAGCTCATCTATCTAC 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 618 CGATGATTTAGAGTGAAGCCGGATATTGTTGTTCCAGGGAATTTGGCGCTTGTGAGTGA 677



Db 782 GAAGGG 787

RESULT 4  
BG351357  
LOCUS 10412 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA EST 01-MAR-2001  
DEFINITION sequence.  
ACCESSION BG351357  
VERSION BG351357.1 GI:13180099  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 677)  
NIELSEN, K.L., CROOKSHANKS, M., EMMERSEN, J. and WELINDER, K.G.  
EST-sequencing of mature potato tuber (Var. Kuras)  
Unpublished (2000)  
Contact: Karen G. Welinder  
Institut for bioteknologi  
Aalborg Universitet  
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kwebio.auc.dk  
Sequenced from the 5' end.  
High quality sequence stop: 677  
POLYA-No.

FEATURES  
source  
1..677  
/organism="Solanum tuberosum"  
/cultivar="Field grown Kuras"  
/db\_xref="taxon:4113"  
/clone\_lib="Mature tuber lambda ZAP"  
/tissue\_type="Tuber"  
/note="Vector: Lambda ZAP"  
BASE COUNT 192 a 102 c 198 g 185 t  
ORIGIN

Query Match 32.9%; Score 568.4; DB 12; Length 677;  
Best Local Similarity 90.9%; Pred. No. 2e-148;  
Matches 616; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 316 GATTCAGTCCGAGAGGAAACCGGCTTTCTATCATCCAGGTTCCAGTCCGAGATAGG 375  
Db 1 GATTCAGTCCGAGAGGAAACCGGCTTTCTATCATCCAGGTTCCAGTCCGAGATAGG 59

QY 376 AATTGTGTGGAATGGAGAAATCAAGAAAGGTGGGAGACAAAGGTGGAATTTTGGCTCT 435  
Db 60 AATTCGATGTGAAGGGAGATTCAGAAAGGTGGGAGACAGAGAGTGGAAATTTGGGTTT 119

QY 436 TTAATTCGTGATCAAGATATTCATGCTTGGTGGATCAAGAATCAAGAGGAGCACT 495  
Db 120 TTAATTCGATGATGAGTGGTATTCAGAGGAGGATTCAGAGGATTCAGATCT 179

QY 496 TTCTCTGTACAGTCCAGTTTGGTGGCTAGCCAGTCCAGAGAAAGTGTCTCATCAGAG 555  
Db 180 TTTCTGTACAGTCCAGTTTGGTGGCTAGCTCCAGTCCAGAAATGGTGTCTCATCAGAG 239

QY 556 AAAAGGTGTATGATGGTATTAAAGCAGCAGCTTTAGTGAAGAGGCACTGAGATCT 615  
Db 240 AAAAGGTGTATGATGGTATTAAAGCAGCAGCTTTAGTGAAGAGGCACTGATCT 299

QY 616 ACCGATGATTAGAGTGAAGCCGGATATGTTGTTCCAGGGAATTTGGGCTTTGAGT 675  
Db 300 ACTGAGGATAGAGTGAAGCCGGATATGTTGTTCCAGGGAATTTGGGCTTTGAGT 359

QY 676 GAAGCATATGATCGTTGGGGAAGTATGTCAGAGATATGCAAGACATTTTACTTAGGA 735  
Db 360 GAAGCATATGATCGTTGGGGAAGTATGTCAGAGATATGCTAAGACATTTTACTTAGGA 419

QY 736 ACCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGCAATATATGTGTGGTGACGG 795  
Db 420 ACCATGCTAATGACTCCAGACAGAGAGAGCTATCTGGCAATATATGTGTGGTGACGG 479

QY 796 AGAAGGATGAGCTTGTGTGATGGCCCTAATGCATCCACATCAACTCCCAAGCTTTAGAT 855  
Db 480 AGAAGTATGAGCTTGTGTGATGGCCCTAATGCATCCACATCAACTCCCAAGCTTTAGAT 539

QY 856 AGGTGGGAGACCGCTGGAGAGATATTTTCAAGTGGGGCCGCAATTTGATATGCTTATGCT 915  
Db 540 AGGTGGGAGACCGCTGGAGAGATATTTTCAAGTGGGGCCGCAATTTGATATGCTTATGCT 599

QY 916 GCTTTATCCGATAGTCTCCAGATTTCTCTGTGATATTCAGCCATTTCAGAGATATGAT 975  
Db 600 GCTTTATCCGATAGTCTTTCCAAATTTCTCTGTGATATTCAGCCATTTCAGAGATATGAT 559

QY 976 GAAGGAATGCGTATGGAC 993  
Db 660 GAAGGAATGCGTATGGAC 677

RESULT 5  
AW442101  
LOCUS EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
DEFINITION clone cLEN21G20 5', mRNA sequence.  
ACCESSION AW442101  
VERSION AW442101.1 GI:6977352  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 686)  
ALCALA, J., VREBALOV, J., WHITE, R., MATERN, A.L., HOLT, I.E., LIANG, F., UPTON, J., HANSEN, T., CRAVEN, M.B., BOWMAN, C.L., AHN, S., RONNING, C.M., FRASER, C.M., MARTIN, G.B., TANKSLEY, S.D. and GIOVANNONI, J.  
Generation of ESTs from tomato fruit tissue  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
1..686  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="cLEN21G20"  
/tissue\_type="pericarp"  
/dev\_stage="red ripe (7-20 days post-breaker)"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; supplier: Giovanni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."  
BASE COUNT 204 a 114 c 182 g 186 t  
ORIGIN

Query Match 32.0%; Score 552.2; DB 10; Length 686;  
Best Local Similarity 87.9%; Pred. No. 7.3e-144;  
Matches 602; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 565 TATGATGTGTTAAAGCAGGCGCTTTAGTGAAGAGGCGCTGAGATCTACCGATGAT 624

Db	2	TATGATGTGGTTTTGAGCGCAGCCCTTGGTGAAGAGGCAACTGAGATCTACCAATGAG	61
QY	625	TTAGAAGTGAAGCCGGATATTTGTTCTCCAGGGAAATTTGGCTTGTGTGAGTGAAGCATAT	684
Db	62	TTAGAAGTGAAGCCGGATATACCTATTCGGGGAAATTTGGCTTGTGTGAGTGAAGCATAT	121
QY	685	GATCGTGTGGCGAAAGTATGTGCAGAGTATGCAAAAGACATTTTACTTTAGGAACCAAGCTA	744
Db	122	GATAGTGTGGTGAAGTATGTGCAGAGTATGCAAAAGAGCTTTACTTTAGGAAGTATGCTA	181
QY	745	ATGACCCAGAGAGAAAGAGCTATCTGGGCAATATATGTGTGGTGCAGAGAACGGAT	804
Db	182	ATGATCCCGAGAGAAAGAGGCTATCTGGGCAATATATGTGTGTCGAAAGAACAGAT	241
QY	805	GAGCTTGTGTATGGCCCTAATCATCTCCACACATACTCCGCAAGCTTTAGATAGTGGGAG	864
Db	242	GAACTTGTGTATGGCCCAACGCATATATTACCCCGCAGCCTTAGATAGTGGGAA	301
QY	865	ACCAGCTCGAAGATATTTTCAGTGGGGGCCAATTTGATATGCTTGATGTGCTTTATCC	924
Db	302	AATAGGCTAGAAGATGTTTTCAATGGGGGGCAATTTGACATGCTCGATGGTCTTTGTC	361
QY	925	GATACTGTCTCAGAGTTTCCCTTTCATATTCAGCCATTCAGAGATATGATTGAAGGAATG	984
Db	362	GATACAGTTTCTAAGCTTCCAGTGTGATATTACGCCATTCAGAGATATGATTGAAGGAATG	421
QY	985	CGTATGGACTTTGTGAAATCCAGATACAAAATTTTCGATGAGCTATATCTATTTGTATC	1044
Db	422	CGTATGGACTTTGAGAAATCCGAGATACAAAATTCGACGAACATATACCTTTATTGTTAT	481
QY	1045	TATGTTGCTGTACTGTAGATTTGATGAGTGTTCACAGTTATGGGTATTTGCACCTGAATCA	1104
Db	482	TATGTTGCTGTACTGTGGTGTGATGAGTGTTCACATTTATGGGTATTCGCCCTTGAATCA	541
QY	1105	AAGGCAACACAGAGAGTATATATATGCTGCTTTGGCTTTAGGGCTTGCAAATCAACTA	1164
Db	542	AAGGCAACACAGAGAGCCTATATATGCTGCTTTGGCTTGGGGATCGCAAACTAATTA	601
QY	1165	ACCAATATACTCAGAGATCTAGGAGAAGTCCAGAAAGAGNAGTATACTTGCCTCAA	1224
Db	602	ACTACATACTCAGAGATGTTGGAGAGATGCCAGAGAGNAGTCTACTTGCCTCAA	661
QY	1225	GATGAATTAGCACAGCGAGGCTCT	1249
Db	662	GATGAATTAACCCAGCGAGGCTCT	686

RESULT	6
LOCUS	BM408984
DEFINITION	EST593311 tomato breaker fruit Lycopersicon esculentum cDNA clone 765 bp mRNA linear EST 22-JAN-2002
ACCESSION	BM408984
VERSION	BM408984.1 GI:18260614
KEYWORDS	EST.
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS	Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai, J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning, C.M., Fraser,C.M., Martin,G.B., Tankalely,S.D. and Giovannonni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002)
TITLE	Contact: CUGI
JOURNAL	Clemson University Genomics Institute
COMMENT	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>

```

This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES             source
    1. .765
        Location/Qualifiers
            /organism="Lycopersicon esculentum"
            /cultivar="TA495"
            /db_xref="taxon:4081"
            /clone="cLEG46P23"
            /clone_lib="tomato breaker fruit"
            /tissue_type="Pericarp"
            /dev_stage="breaker"
            /lab_host="SOLR"
            /note="Vector: pBluescriptSkmCudapt; Site.1: Ecor1;
            Site.2: XhoI; supplier: Boyce Thompson Institute.
            sequencing: The Institute for Genomic Research. Fruit
            were harvested at the breaker stage (first sign of
            lycopenic accumulation on the blossom end of fruit). Fruit
            were cut in half and the seeds and locules were discarded
            prior to freezing the pericarp."
    237 a      122 c      202 q      204 t
BASE COUNT

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BASE COUNT	237 a	122 c	202 g	204 t	
ORIGIN	prior to freezing the particip.				
Query Match	31.9%	Score 551.2	DB 13	Length 765	
Best Local Similarity	86.1%	Pred No 1.5e-143			
Matches 634	Conservative 0	Mismatches 98	Indels 4	Gaps 2	
Qy	625	TTAGAAGTGAAGCGGGATATGTTGTTCCAGGGGAATTTGGCTGTGTGAGTGAAGCATAT	684		
Db	1	TTAGAAGTGAAGCGGATATACCTATTTCGCGGAATTTGGCTGTGTGAGTGAAGCATAT	60		
Qy	685	GATCGTTGTGGCGAAGTATGTGCAGAGATGTGCAAGACATTTTACTTTAGNACCAAGCTA	744		
Db	61	GATAGGTGTGGTGAAGTATGTGCAGAGATGTGCAAGACGTTTAACTTTAGAACTATGCTA	120		
Qy	745	ATGACCCCGACAGAGAAGACGCTATCTGGGCAATATATGTGTGGTCAGGAGAACGGAT	804		
Db	121	ATGACTCCGAGAGAAGAGGGCTATCTGGGCATATATGTGTGTCAGAGAACAGAT	180		
Qy	805	GAGCTTTGTGATGCCCTATATGCATCCACATAACTCCGCAAGCTTTTAGATAGTGGGAG	864		
Db	181	GAACTTTGTGATGCCCAACGACATCATATATTACCCGCGAGCTTTAGATAGTGGGAA	240		
Qy	865	ACCAGGTGGAAGATATTTTCAGTGGGCGGCATTTTCATATGCTTGATGCTGCTTTATCC	924		
Db	241	AATAGGCTAGAAGATGTTTCAATGGGCGGCCATTTGACATGCTCGATGGTGTGCTTGTCC	300		
Qy	925	GATACTGCTCCAGATTTCCCTGTTGATATTACAGCCATTCAGAGATATGATTGAAGGAATG	984		
Db	301	GATACAGTTTCTAATTTCCAGTTGATATTACGCCATTCAGAGATATGATTGAAGGAATG	360		
Qy	985	CGTATGACTGTGGAAATCCAGATACAAACTTTTCATGAGCTATATCTCTATTTGTTAC	1044		
Db	361	CGTATGACTTTGAAAAATCGAGATACAAAACCTTCGACGAACCTATACCTTTATTTGTTAT	420		
Qy	1045	TATCTTCTGCTAGTCTAGGATTCATCAGTGTTCACAGTTATGGGTATTCACCTTGAATCA	1104		
Db	421	TATCTTCTGCTAGCGTTGGGTGATGAGTGTTCCAATATGGGTATTCGCCCTTGAATCA	480		
Qy	1105	AAGGCAACAACAGAGAGTGATATAATGCTGCTTTGGCTTTAGGGCTTGCAAAATCAACTA	1164		
Db	481	AAGGCAACAACAGAGAGCGTATATAATGCTGCTTTGGCTCTGGGGATTCGCAATCAATTA	540		
Qy	1165	ACCAATATACTCAGAGATGTAGGAGAAGATGCCAGAGAAGAGAGTATACTTGCCTCAA	1224		
Db	541	ACTAACATCTCAGAGATGTTGGAGAAGATGCCAGAGAAGGAAGAGTCTACTTGCCTCAA	600		
Qy	1225	GATGAATTAGCACAGGCGGGCTCTCCGACGAAGACATA-TTTGCTGGAAGAGTACTGA	1283		
Db	601	GATGAATTAGCACAGGCGAGGTCTATCCGATGAAGATATATTTGCTGGAAGGGTGCACGA	660		
Qy	1284	TAACTGGAGGAACPTTTATGAAGAAACAAATTCACAGGCGGAGGAAATTTCTTTGATGAGTC	1343		

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Db 661 TAAATGGAGAATCTTTATGAGAACAA---TACTAGGCGAAGAAAGTCTTTGATGAGCA 717
QY 1344 AGAGAAGGTGTCA 1359
Db 718 GAGAAAGCGTGACAGA. 733

RESULT 7
LOCUS BM409200 682 bp mRNA linear EST 22-JAN-2002
DEFINITION EST383527 tomato breaker fruit Lycopersicon esculentum cDNA clone
ACCESSION cLEG47J1.5' end, mRNA sequence.
VERSION BM409200
KEYWORDS EST.
SOURCE EST.
ORGANISM tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 682)
REFERENCE 1
AUTHORS Alcalá,J., Vrebalov,J., White,R., Visions,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage. (2002)
Unpublished (2002)
CONTACT: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..682
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato breaker fruit"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOL"
/note="Vector: pBluescriptSMCadapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
BASE COUNT 217 a 114 c 173 g 178 t
ORIGIN

Query Match 31.3%; Score 541.2; DB 13; Length 682;
Best Local Similarity 87.1%; Pred. No. 9.1e-141;
Matches 594; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 706 GCAGAGTATGCAAGACATTTTACTTAGGACCAAGCTAATGACCCAGAGAGAAGA 765
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Db 1 GCAGAGTATGCAAGACGTTTACTTAGGACCAAGCTAATGACCTCCGAGAGAAGG 60
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QY 766 GCTATCTGGCATATATGTTGGTGCAGGAGACCGATGAGTTTGTATGCCCTAAT 825
|||||
Db 61 GCTATCTGGCAATATATGTTGGTGCAGAGAACAGATGAATCTTTGATGGCCCAAC 120
|||||

QY 826 GCATCCACATACTCCGCAAGCTTTAGATAGTGGGAGACCGCTGGAAGATATTTTC 885
|||||
Db 121 GCATCATATATTACCCGCGAGCTTAGATAGTGGGAAATAGGCTAGGAAGATGTTTC 180
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QY 886 AGTGGCGGCCATTTGATGCTTGTGCTTTCGATGCTTTCGATGCTTCCAGATTTCT 945
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Db 181 AATGGCGGCCATTTGACATGCTCGATGGTGGCTTTGTCCGATACAGTTTCTAATTTCCA 240
QY 946 GTTGATATTTCAGCCATTTCAGAGATATGATTGAAGGAATCGGTATGGACTTTGTGAAATCC 1005
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Db 241 GTTGATATTTCAGCCATTTCAGAGATATGATTGAAGGAATCGGTATGGACTTTGAGAAAATCG 300
|||||

QY 1006 AGATACAAAACITTCGATGAGCTATATCTCTATTGTTTACTATGTTGCTGCTACTGTAGGA 1065
|||||
Db 301 AGATACAAAACITTCGACCAACTATACCTTTATTGTTTATTGTTGCTGCTACTGTAGGG 360
|||||

QY 1066 TTGATGAGTGTTCACGTTATGCGTATTGACCTGAATCAAGCAACCAACAGAGAGTGA 1125
|||||
Db 361 TTGATGAGTGTTCACGTTATGCGTATTGCGCTTGAATCAAGCAACCAACAGAGAGCGTA 420
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QY 1126 TATAATGCTGCTTTGGCTTTAGGGCTTGAATCAATCAACTAACCAATATPACTCAGAGATGA 1185
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Db 421 TATAATGCTGCTTTGGCTTGGGATCGCAATCAATTAACATACTCAGAGATGTT 480
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QY 1186 GGAGAGATGCCAGAGAGAGAGATATGCTTGCCTCAAGATGAATTAAGCACAGGAGGG 1245
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Db 481 GGAGAGATGCCAGAGAGAGAGATGCTTGCCTCAAGATGAATTAATCAGAGGAGGT 540
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QY 1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTGAATGAGTGGAGAACTTTATCAAG 1305
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QY 1306 AAACAATTCAGAGGCGAGGAGAAATTTCTTTGATGAGTCAGAGAAAGGTGTCACAGACTG 1365
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Db 601 AAACAATACATAGGCGCAAGAAAGTTCTTTGATGAGCAGAGAAAGGCGTGACAGAAATG 660
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QY 1366 GACTCTGCTAGTAGTAGGCTG 1387
Db 661 AGCTCAGCTAGTAGTAGTCCCTG 682

RESULT 8
LOCUS AW442407 672 bp mRNA linear EST 18-MAY-2001
DEFINITION EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
ACCESSION AW442407
VERSION AW442407
KEYWORDS EST.
SOURCE EST.
ORGANISM tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 672)
REFERENCE 1
AUTHORS Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..872
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/cultivar="TA496"
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/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the

```

blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT	212 a	112 c	170 g	178 t	
ORIGIN					
Query Match	30.8%	Score 532.8;	DB 10;	Length 672;	
Best Local Similarity	87.1%	Pred. No. 2.1e-138;			
Matches 585;	Conservative 0;	Mismatches 87;	Indels 0;	Gaps 0;	
QY 719	AGACATTTTACTTAGAACCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAA	778			
Db 1	AGACGTTTAACTTAGCACTAATGCTCCGAGAGAGAGAGGCTATCTGGGCAA	60			
QY 779	TATATGTGTGGTGCAGGAGCGGATGAGCTGTGTGATGGCCCTAATGCATCCCAATAA	838			
Db 61	TATATGTGTGGTGCAGGAGCGGATGAGCTGTGTGATGGCCCAACGCATCATATATA	120			
QY 839	CTCCCAAGCTTTAGATAGGTGGGAGACGAGCTGGAAGATATTTTCAGTGGCGGCCAT	898			
Db 121	CCCCGCGAGCTTAGTAGGTGGGAATAGCTAGAGATGTTTTCATGGCGGCCAT	180			
QY 899	TGTATAGCTTGATGCTGCTTTATCCGATACCTGCTCCAGATTTCTCTGTGATATTCAGC	958			
Db 181	TTGACATGCTGATGCTGCTTTGTCGGATACAGTTTCACTTCAGTTGATATTCAGC	240			
QY 959	CATTGAGATATGATTGAGAAATGCGTATGAGCTTGTGGAATCCAGATACAAACTT	1018			
Db 241	CATTGAGATATGATTGAGAAATGCGTATGAGCTTGTGGAATCCAGATACAAACT	300			
QY 1019	TCGATGAGCTATATCTTATTTACTATGTTGCTGCTACTGATGAGGATGATGAGTTC	1078			
Db 301	TCGAGCACTATACCTTTATGCTTATTTATGTTGCTGCTAGGTTGGTGGTGGTTC	360			
QY 1079	CAGTTATGGGTATTCACCTGAATCAAGGCAACACAGAGAGTGTATATATGCTGCTT	1138			
Db 361	CAATTATGGGTATTCGCTGAATCAAGGCAACACAGAGAGCTATATATGCTGCTT	420			
QY 1139	TGGCTTTAGGCTTGCATCACTAATCACTAATCACTAATCACTAATCACTAATCACTA	1198			
Db 421	TGGCTTTAGGCTTGCATCACTAATCACTAATCACTAATCACTAATCACTAATCACTA	480			
QY 1199	GAGAGGAGAGTATATCTGCTCAAGATGAATAGCAGAGAGAGGCTCTCCGAGAG	1258			
Db 481	GAGAGGAGAGTATATCTGCTCAAGATGAATAGCAGAGAGAGGCTCTCTCCGAGAG	540			
QY 1259	ACATATTTGCTGGAAGAGTACTGATAAGTGGAGGAATTTATGAAGAAACAAATTCAGA	1318			
Db 541	ATATATTTGCTGGAAGAGTACCAGATGAATAGGAGATCTTTATGAAGAAACAAATACATA	600			
QY 1319	GGGCGAGGAATCTTTGATGAGTACAGAAAGGTTGCACAGACTGGACTCTGCTAGTA	1378			
Db 601	GGGCGAGGAATCTTTGATGAGTACAGAAAGGTTGCACAGACTGGACTCTGCTAGTA	660			
QY 1379	GATGGCTGCTGT	1390			
Db 661	GATTCCTGTAT	672			
RESULT 9	BE433198				
LOCUS	EST399727	642 bp	mRNA	linear	EST 18-MAY-2001
DEFINITION	tomato breaker fruit; TIGR Lycopersicon esculentum cDNA				
ACCESSION	BE433198				
VERSION	BE433198.1				
KEYWORDS	EST				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 642)  
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J., and Tanksley, S.D.

Generation of ESTs from tomato fruit tissue, breaker stage  
Unpublished (2000)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
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/dev\_stage="breaker"  
/lab\_host="SOLR"  
/note="Vector: pBluescriptSKmCuadapt; Site\_1: EcoRI; Site\_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."  
BASE COUNT 194 a 103 c 167 g 178 t

Query Match	30.2%	Score 522;	DB 10;	Length 642;	
Best Local Similarity	88.3%	Pred. No. 2.2e-135;			
Matches 567;	Conservative 0;	Mismatches 75;	Indels 0;	Gaps 0;	
QY 660	TTTGGGCTTGTGAGTGAAGCATATGATGCTGTTGTGCGAAGTATGTGCGAGATATGCAA	719			
Db 1	TTTGGGCTTGTGAGTGAAGCATATGATGCTGTTGTGCGAAGTATGTGCGAGATATGCAA	60			
QY 720	GACATTTTACTTAGGAACCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAAT	779			
Db 61	GAGCTTTACTTAGGAACCTATGCTAATGACTCCGAGAGAGAGAGGCTATCTGGGCAAT	120			
QY 780	ATATGCTGCTGAGAGAACCGATGAGCTTGTGATGGCCCTTAATGCTCCACATAAC	839			
Db 121	ATATGCTGCTGAGAGAACCGATGAGCTTGTGATGGCCCTTAATGCTCCACATAAC	180			
QY 840	TCGCAAGCTTTAGATAGTGGGAGACGAGCTGGAAGATATTTTCAGTGGGCGGCATT	899			
Db 181	CCGCGAGCTTTAGATAGTGGGAGAAATAGGCTAGAGATGTTTTCAGTGGGCGGCATT	240			
QY 900	TGATATGCTGATGCTGCTTTATCCGATACCTGCTCCAGATTTCCCTGTTGATATTCAGCC	959			
Db 241	TGACATGCTGATGCTGCTTTTCCGATACAGTTTCTAATTCAGTTCGATATTCAGCC	300			
QY 960	ATTCAGAGATATGATTGAAGGAATCGTATGGACTTGTGGAATCCAGATACAAAATTTT	1019			
Db 301	ATTCAGAGATATGATTGAAGGAATCGTATGGACTTGTGGAATCCAGATACAAAATTTT	360			
QY 1020	CGATGAGCTATATCTTACTTGTACTATGCTGCTGCTAGGATGATGAGTGTTC	1079			
Db 361	CGACGAACCTATACCTTTATGTTATTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420			
QY 1080	AGTTATGGTATGTCACCTGAATCAAGGCAACACAGAGAGTGTATATATGCTGCTTT	1139			
Db 421	AATTATGGTATGTCACCTGAATCAAGGCAACACAGAGAGTGTATATATGCTGCTTT	480			
QY 1140	GGCTTTAGGCTTGCATAACTCACTAACATATATCTCAGAGATGTAGGAGAGATGCCAG	1199			
Db 481	GGCTTTAGGCTTGCATAACTCACTAACATATATCTCAGAGATGTAGGAGAGATGCCAG	540			



QY 1200 RAGAGGAGAGTATCTTGCCTCAGATGAATTAGCACAGCAGGGCTCTCCGACGAGA 1259  
 DB 541 RAGAGGAGAGTATCTTGCCTCAGATGAATTAGCACAGCAGGGCTCTCCGATGAAGA 600  
 QY 1260 CATATTTCTGGAAGAGTACTGATAGTGAGGAGAACTTTAT 1301  
 DB 601 TATATTTCTGGAAGGTTGACCGATAATGAGAACTTTAT 642

RESULT 10  
 AW222027  
 LOCUS  
 DEFINITION EST298838 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
 clone cLEN6L15, mRNA sequence.  
 ACCESSION AW222027  
 VERSION AW222027.1 GI:5533711  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Lycopersicon esculentum  
 tomato.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 676)  
 Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Holt, I. E., Liang, F.,  
 Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Ronning, C. M.,  
 Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.  
 Generation of ESTs from tomato fruit tissue  
 Unpublished (1999)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

## FEATURES

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Location/Qualifiers

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/organism="Lycopersicon esculentum"

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/clone="cLEN6L15"

/tissue\_type="pericarp"

/dev\_stage="red ripe (7-20 days post-breaker)"

/note="vector: p Bluescript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; supplier: Giovannoni; Fruit were tagged at the

breaker stage. (first sign of lycopene accumulation on the

blossom end of the fruit) and harvested 7 days

post-breaker (fully red-ripe), 10 days post breaker, and

20 days post-breaker (over-ripe). 20 day fruit which

showed external or internal signs of pathogenesis were

discarded. Fruit were cut in half and the seeds and

locules were discarded prior to freezing the pericarp."

214 a 118 c 165 g 179 t

## BASE COUNT

ORIGIN

Query Match 29.8%; Score 515.8; DB 10; Length 676;  
 Best Local Similarity 85.5%; Pred. No. 1.2e-133;  
 Matches 574; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 808 CTTGTGTGATGGCCCAATGATCCACATCTCCGCAAGCTTTAGATAGTGGGAGACC 867  
 DB 2 CTTGTGTGATGGCCCAAGCATCATATATACCCCGGAGCCTTAGATAGTGGGAAAT 61  
 QY 868 AGGCTGGAAGATATTTCAGTGGGGGCCATTGTATGCTTGTGATGCTTTATCCGAT 927  
 DB 62 AGGCTAGAAGATGTTTCAATGGGGGCCATTGTGACATGCTCGATGGTCTTGCCTGAT 121  
 QY 928 ACTGCTCCAGATTTCTGTTGATATTTCAGCCATTTACAGATATGATTGAAGGAATGCGT 987  
 DB 122 ACAGTTTCTTAATTTCCAGTTTGATATTCAGCCATTTACAGATATGATTGAAGGAATGCGT 181

QY 988 ATGCACTTGTGGAATCCAGATACAAAACCTTCGATGAGCTATATCTCTATTGTACTAT 1047  
 DB 182 ATGCACTTGTGGAATCCAGATACAAAACCTTCGAGCAACTATACCTTTATTGTATTAT 241  
 QY 1048 GTTCTGCTACTGTAGGATTGATGAGTTCACAGTTATGGGTATTTGCACTTGAATCAAG 1107  
 DB 242 GTTCTGCTAGGTTGGTTCATGAGTTCCTCAATTTATGGGTATCGCCCTCAATCAAG 301  
 QY 1108 GCAACAACAGAGAGTGTATATAATGCTCTTGGCTTTTAGGGCTTGGCAATCAATCAAC 1167  
 DB 302 GCAACAACAGAGAGCTATATAATGCTCTTGGCTTGGGATCGCAATCAATTAAT 361  
 QY 1168 AATATCTACAGAGTGTAGGAGAGATCCAGAGAGAGAGATGATCTTGCCTCAAGAT 1227  
 DB 362 AACATCTACAGAGTGTGGAGAGATCCAGAGAGAGAGATGATCTTGCCTCAAGAT 421  
 QY 1228 GAATTAGCACAGGAGGCTCTCCGACGAGACATATTTGCTGGAGAGTACTGATGAAG 1287  
 DB 422 GAATTAGCACAGGAGGCTCTATCCGATCAAGATATATTTGCTGGAGAGTACTGATGAAG 481  
 QY 1288 TGGAGGAACTTTATGAAGAAACAAATTCAGAGGGCGAGAAATCTTTGATGAGTCAGAG 1347  
 DB 482 TGGAGAACTTTATGAAGAAACAAATACATAGGGCAAGAAATCTTTGATGAGTCAGAG 541  
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 DB 542 AAAGGTGTACAGAAATTTGAGTCTAGTCTAGTATGCTGATGGGATCTTTGGTCTGTTG 601  
 QY 1408 TATCGCAAGATTTGGACGAGATTGAAGCCCAACGACTACAACTTTCACAGAGGAGGCT 1467  
 DB 602 TACCGCAAGATTTAGATGAGATTGAAGCCCAATGACTACAACTTTCACAAAGAGAGCA 661  
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RESULT 11  
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 ACCESSION BM412533  
 VERSION BM412533.1 GI:18264163  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 634)  
 Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S. A., Tsai,  
 J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning,  
 C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D., and Giovannoni, J.  
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)  
 Unpublished (2002)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute  
 Seq primer: T3.  
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 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLEG60I14"  
 /tissue\_type="pericarp"

## FEATURES

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Location/Qualifiers

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/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEG60I14"

/tissue\_type="pericarp"



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/dev_stage="breaker"
/lab_host="SOLR"
/site="Vector: pbluescriptskmuadapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
BASE COUNT      200 a 105 c 160 g 169 t
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Best Local Similarity 87.6%; Pred. No. 1.1e-128;
Matches 556; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 706 GCAGAGTATGCAAGACATTTTACTTAGCAACCAAGCTAATGACCCAGAGAGAGAAGA 765
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QY 766 GCTATCTGGCAATATATGTGTGGTCAGGAGACGGATGAGCTTTGTGATGGCCCTAAT 825
DB 61 GCTATCTGGCAATATATGTGTGGTCAGGAGACAGATGAAGTGTGTGATGGCCCAAC 120
QY 826 GCATCCACATTAACCCCAAGCTTTAGATAGTGGGAGACAGCTGGAGATATTTTC 885
DB 121 GCATCATATATTACCCCGGACCTTTAGATAGTGGGAGAAATAGGCTAGAAGATGTTTC 180
QY 886 AGTGGCGGCCATTTGATATGCTTGTATGCTGCTTTATCCGATACGTGTCTCCAGATTGCT 945
DB 181 AATGGCGGCCATTTGATATGCTGCTGCTTTGTCGATACAGTTCTTAACCTTTCA 240
QY 946 GTTGATATTACCCATTCAGAGATATGATGAAGAAATGCCPATGGACTTTGGAAATCC 1005
DB 241 GTTGATATTACCCATTCAGAGATATGATGAAGAAATGCCPATGGACTTTGAGAAATCG 300
QY 1006 AGATACAAACTTTGATGAGTATATCTTACTTACTTACTTGTGCTGGTACTAGGA 1065
DB 301 AGATACAAACTTTGATGAGTATATCTTACTTACTTACTTGTGCTGGTACTAGGA 360
QY 1066 TTGATGAGTTTCCAGTTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
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QY 1126 TATATGCTGCTTTGGCTTTAGGCTTGCAATCAACATCAACATATATCTACAGATGTA 1185
DB 421 TATATGCTGCTTTGGCTTTAGGCTTGCAATCAACATCAACATATATCTACAGATGTA 480
QY 1186 GGAGAGATGCCAGAGAGAGATATATCTGCTCAAGATGAATTAGCAGACAGCAGG 1245
DB 481 GGAGAGATGCCAGAGAGAGATATATCTGCTCAAGATGAATTAGCAGACAGCAGG 540
QY 1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTGAATGATGATGATGATGATGATGATGAT 1305
DB 541 CTATCCGATGAGATATATTTGCTGGAAGGTTGACCGATGAATGAGATATCTTATGAG 600
QY 1306 AAACAAATTCAGAGGCGGAGGAAATCTTTTGATGA 1340
DB 601 AAAC-AATACATAGGGGAGAGAGTCTTTTGATGA 634

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RESULT 12
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LOCUS
DEFINITION B1921390 599 bp mRNA linear EST 17-OCT-2001
EST541293 tomato callus Lycopersicon esculentum cDNA clone cLEC73K6
5' end, mRNA sequence.
ACCESSION B1921390
VERSION B1921390.1 GI:16217418
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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Asteridae: euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 599)
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai
, J., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin
, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
Source 1.599
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC73K6"
/clone_lib="tomato callus"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
BASE COUNT      170 a 89 c 178 g 162 t
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Query Match      28.2%; Score 487.2; DB 13; Length 599;
Best Local Similarity 89.3%; Pred. No. 1.3e-125;
Matches 536; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 275 TTTCTCCACATTCGAGGTCGAAATGGGACAGGATTTGGATTTCAGTCCGAGAGGAA 334
DB 1 TTTCTCCGAATTCGAGGTCCTACGGGACAGGATTTGGATTTCAGTCCGAGAGGAA 60
QY 335 ACCGCGTCTTTTATCATCCAGGTTCTAGCTCGAGATAGGAATTTGATGTCGAATGGA 394
DB 61 ACCGGGTTTGGAAATCATCCAGTTCCCATCTCGGATAGGAATTCGATGGAAGGAG 120
QY 395 GAATCAAGAAAGTGGGACAAAGTGGAAATTTTGGCTCTTTAAATGCTGATCCAGAT 454
DB 121 GATTCAAGAAAGTGGGACAAAGTGGAAATTTTGGGTTTAAATGCGAGATTTGAGAT 180
QY 455 ATTCATGCTTTGGTGGATCAAGAACTGAAAGGGAAGCACTTTCTCTGTACACTCCAGTT 514
DB 181 ATTCGTTTATGAGATCAAGAACTGAGAAATGGAAGGAGTTTCTCTGACAGCTAGT 240
QY 515 TGGTGGCTAGCCAGCTGGAGAAATGACTGTGTATCATCAGAGAAAGGTTATGATGTGG 574
DB 241 TGGTGGCTAGTCCAGCTGGAGAAATGGCTGTGTATCATCAGA-AAGGATGATGAGTGG 299
QY 575 TATTAAAGCAGCAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTAGAGTGA 634
DB 300 TATTAAAGCAGCAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTAGAGTGA 359
QY 635 AGCCGGATATTTCTTCCAGGGAATTTGGGCTTTGTTGAGTGAAGCATATGATCGTGTG 694
DB 360 AGCCGGATATTTCTTCCGGGTAATTTGGGCTTTGTTGAGTGAAGCATATGATCGTGTG 419
QY 695 GCGAAGTATGTCAGAGATGCAAGACATATTTTACTTAGGAACCAAGCTAATGACCCAG 754
DB 420 GCGAAGTATGTCAGAGATGCAAGACATATTTTACTTAGGAACCAAGCTAATGACCCAG 479
QY 755 AGAGAAGAGAGCTATCTCGGCAATATATGTGTGTGAGGAGAGACGATGAGCTTTGTTG 814

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Db 480 ACAGAGAGAGCTATCTGGCCATATATGTGTGGTCAGAGAACTGAAGCTTTGTTG 539
QY 815 ATGGCCCTAATGCATCCACATAACTCCCAAGCTTTAGATAGGTGGGAGACACAGGCTGG 874
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RESULT 13
BE460889
LOCUS
DEFINITION EST412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE460889
VERSION BE460889
KEYWORDS EST.
SOURCE BE460889.1 GI:9505191
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 600)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
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Location/Qualifiers
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/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSMCudapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 178 a 99 c 157 g 166 t
ORIGIN
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Best Local Similarity 88.2%; Pred. No. 2.2e-125; Indels 0; Gaps 0;
Matches 529; Conservative 0; Mismatches 71;
QY 650 TTCCAGGGAATTTGGCTTTGAGTGAAGCATATGATGTTGTGGCGAGTATGTGCAG 709
Db 1 TTCCGGGGAATTTGGCTTTGAGTGAATCATATGATAGTGTGTGAGTGTGTGCAG 60
QY 710 AGTATGCAAGACATTTTACTTAGGAACCAACAGCTAATGACCCAGAGAGAGAAAGACTA 769
Db 61 AGTATGCAAGACATTTTACTTAGGAACCAACAGCTAATGATGCTCCGAGAGAAAGGCTA 120
QY 770 TCTGGGCAATATATGTGTGGTCAGGAGACGATGCTGTGTGATGGCCCTAATGCGAT 829
Db 121 TCTGGGCAATATATGTGTGGTCAGGAGACAGATGCTGTGTGATGGCCCAAGCGAT 180
QY 830 CCCCACTAATCCGCAAGCTTTAGATAGTGGGAGACCAAGCTTGGGAAGATATTTTCAGTG 889
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QY 890 GCGGGCCATTTGATATGCTGTGATGCTGCTTTATCCGATACTGTCTCCAGATTTCTGTTG 949
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QY 950 ATATTTCAGCCATTTCAGAGATATGATTGAAGGAATGCTATGGACTTGTGGAAATCCAGAT 1009
Db 301 ATATTTCAGCCATTTCAGAGATATGATTGAAGGAATGCTATGGACTTGTGGAAATCCAGAT 360
QY 1010 ACAAACCTTTTCGATGAGCTATATCTCTATTGTTTACTATGTTGCTGCTAGGATTGA 1069
Db 361 ACAAACCTTTTCGAGAACTATACCTTTATTGTTTACTATGTTGCTGCTAGGATTGA 420
QY 1070 TGAGTGTTCAGCTATGCTGATGCTGACCTTGAATCAAGGCAACACAGAGAGTGTATATA 1129
Db 421 TGAGTGTTCAGCTATGCTGATGCTGACCTTGAATCAAGGCAACACAGAGAGTGTATATA 480
QY 1130 ATGCTGCTTTGGCTTTAGGCTTTCAGAACTCAACTAACCAATATCTACAGAGATGTAGGAG 1189
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QY 1190 AAGATGCCAGAGAGAGAGATGATGCTGCTCAAGATGAATTAGCACAGGCGAGGCTCT 1249
Db 541 AAGATGCCAGAGAGAGAGATGCTGCTCAAGATGAATTAGCACAGGCGAGGCTCTAT 600

RESULT 14
BE432511
LOCUS
DEFINITION EST399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE432511
VERSION BE432511
KEYWORDS EST.
SOURCE BE432511.1 GI:9430354
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 623)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
Location/Qualifiers
1..623
/organism="Lycopersicon esculentum"
/db_xref="TA496"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 191 a 101 c 164 g 167 t
ORIGIN
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Best Local Similarity 87.2%; Pred. No. 1.6e-124; Indels 4; Gaps 1;
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